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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Wed Aug 16 09:45:05 2000; MasPar time 5.58 Seconds 560.903 Million cell updates/sec MPsrch\_pp

Tabular output not generated.

Title:

>US-09-427-873-2
(1-101) from US09427873.pep
683
1 LGKFSQTCYNSAIQGSVLTS.....STKINLDDHIANIDGTLKYE 101 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

85661 seqs, 30989116 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Mean 39.367; Variance 62.654; scale 0.628 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1		ď			COLUMNICO		
	Score	Query	Query Match Length	BB	QI	Description	Pred. No.
-	664	97.2	101		CVN_NOSEL	CYANOVIRIN-N (CV-N).	3.44e-138
~	103	15.1	327	-	ACCO_DORSP	1-AMINOCYCLOPROPANE-1-	3.79e-04
ო	92	13.5	416	Н	RHLA_PANTR	RH-LIKE PROTEIN IA (RH	2.79e-02
4	91	13.3	416	Н	RHD_HUMAN	BLOOD GROUP RH(D) POLY	4.06e-02
ഗ	91	13.3	505	-	ACHB_BOVIN	ACETYLCHOLINE RECEPTOR	4.06e-02
9	96	13.2	416	Н	RHL_MACMU	RH-LIKE PROTEIN (RHESU	5.89e-02
7	89	13.0	416	٦	RHLR_PANTR	RH-LIKE PROTEIN IIR (R	8.54e-02
ω	86	12.6	353	-	RHL_HYLPI	RH-LIKE PROTEIN (RHESU	2.55e-01
6	98	. 12.6	392	Н	VATC_YEAST	VACUOLAR ATP SYNTHASE	2.55e-01
10	86	12.6	1014	ч	NANH_CLOSE	SIALIDASE PRECURSOR (E	2.55e-01
11	82	12.4	223	٦	AOP2_MOUSE	ANTIOXIDANT PROTEIN 2	3.65e-01
12	82	12.4	223	-	AOP2_HUMAN	ANTIOXIDANT PROTEIN 2	3.65e-01
13	82	12.4	501	Н	ACHB_RAT	ACETYLCHOLINE RECEPTOR	3.65e-01
14	82	12.4	501	Н	ACHB_HUMAN	ACETYLCHOLINE RECEPTOR	3.65e-01
15	85	12.4	501	Н	ACHB_MOUSE	ACETYLCHOLINE RECEPTOR	3.65e-01
16	84	12.3	223	Н	AOX2_RAT	ANTIOXIDANT PROTEIN 2	5.21e-01
17	83	12.2	223	Н	AOP2_BOVIN	ANTIOXIDANT PROTEIN 2	7.42e-01
18	83	12.2	416	Н	RHLD_GORGO	RHESUS-LIKE PROTEIN.	7.42e-01
19	82	12.0	717	Н	CLA1_ARATH	PROBABLE 1-DEOXYXYLULO	1.05e+00
20	81	11.9	320	Н	ACC3_CUCME	1-AMINOCYCLOPROPANE-1-	1.49e+00
21	81	11.9	419	Н	HFLK_ECOLI	HFLK PROTEIN.	1.49e+00
22	81	11.9	683	-1	VTER_HSVSA	PROBABLE DNA PACKAGING	1.49e+00
23	. 80	11.7	450	Н	ENV2_ECOLI	OSMOLARITY SENSOR PROT	2.10e+00

•																					
2.10e+00	2.10e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	2.95e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00	4.13e+00
NEURONAL ACETYLCHOLINE	SECRETOGRANIN II PRECU	HYPOTHETICAL CALCIUM-B	PROBABLE ISOPENTENYL-D	1-AMINOCYCLOPROPANE-1-	RH-LIKE PROTEIN IIF (R	SENSORY RHODOPSIN II T	B-CELL LYMPHOMA 6 PROT	SYNAPTONEMAL COMPLEX P	CELL DIVISION CONTROL	ZINC FINGER PROTEIN HR	P4 PROTEIN.	CARBONIC ANHYDRASE VI	1-AMINOCYCLOPROPANE-1-	RH-LIKE PROTEIN IC (RH	FLAGELLAR HOOK PROTEIN	OSMOLARITY SENSOR PROT	OSMOLARITY SENSOR PROT	LETHAL(1)DISCS LARGE-1	VIRULENCE SENSOR PROTE	VIRULENCE SENSOR PROTE	190 KDA ANTIGEN PRECUR
ACHP_CHICK	SG2_RANRI	YGK6_YEAST	IDI_RHOSH	ACC1_CUCME	RHLF_PANTR	HTR2_NATPH	BCL6_HUMAN	SCP1_MESAU	CC47_YEAST	HRX_MOUSE	VP4_SBMV	CAH6_SHEEP	ACCO_PERAE	RHLC_GORGO	FLGE_BORBU	ENVZ_SALTY	ENVZ_SALTI	DLG1_DROME	BVGS_BORBR	BVGS_BORPA	190K RICRI
Н	Н	~1	٦	٦	Ţ	٦	-	Н	Н	٦	٦	٦	ч	Н	Н	Н	Н	H	Н	~	~
470	601	149	177	318	416	534	206	845	845	3866	185	307	320	416	442	450	450	960	1238	1238	2249
11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4
80	80	79	79	79	79	79	79	79	79	79	7.8	78	78	78	78	78	78	78	78	78	78
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45
	NEURONAL ACETYLCHOLINE	470 1 ACHP_CHICK NEURONAL ACETYLCHOLINE 601 1 SG2_RANRI SECRETOGRANIN II PRECU	470 1 ACHP CHICK NEDRONAL ACETYLCHOLINE 601 1 SGLEPORANI SECRETOGRANIN II PRECU 149 1 YGK6_YEAST HYPOTHETICAL CALCIUM-B	80 11.7 470 1 ACHP_CHICK NEURONAL ACETYLCHOLINE 80 11.7 601 1 SG2_RANRI SECRETOGRANIN II PRECU 79 11.6 149 1 YGK6_TSFAY IYPOTHETICAL CALCIUM-B 79 11.6 177 1 IDI_RHGSH PROBABLE ISOPENTENYL-D	80 11.7 470 1 ACHP_CHICK NEURONAL ACETYLCHOLINE 80 11.7 601 1 SG2_RANNI SECRETOGRANIN II PRECU 79 11.6 149 1 VGK6_YEAST HYPOTHETICAL CALCIUM-B 79 11.6 171 101_KHOSH PROBABLE ISOPENTENYL-D 79 11.6 171 ACCI_CUCME 1-AMINOCYCLOPROPANE-1-	80   11.7   470   1 ACHP_CHICK NEURONAL ACETYLCHOLINE   80   11.7   601   1 SG2_RANR1   SECRETOGRANIN II PRECU   79   11.6   149   1 YOK6_YEAST   PYOPHETICAL CALCIUM-B   79   11.6   177   1 IDI_RHOSH   PYOBABLE ISOPEWIENYL-D   79   11.6   318   1 ACCI_CUCMB   1-AMINOCYCLOPROPANE   1.6   18   18 HLF_PANTN   RH-LIKE PROTEIN IIF (R	80   11.7   470   1 ACHP_CHICK NEURONAL ACETYLCHOLINE     80   11.7   601   1 SG2_RANRI SECRETOGRANINI II PRECU     79   11.6   149   1 YER6_TEAST HYPOTHETICAL CALCIUM-B     79   11.6   177   1 IDI_RHOSH PROBABLE ISOPENTENYL-D     79   11.6   416   1 RHLF_PANTR RH-LIKE PROTEIN IIF (R     79   11.6   334   1 HTR2_NATPH SENSORY RHODOPSIN III T	80 11.7 470 1 ACHP_CHICK NEURONAL ACETYLCHOLINE 80 11.7 601 1 SG2_RANRI SECRETOGRANIN II PRECU 79 11.6 149 1 VGK6_PEAST HYPOTHETICAL CALCIUM-B 79 11.6 177 1 IDI_RHOSH PROBABLE ISOPENTENYL-D 79 11.6 318 1 ACCI_CUCME 1-AMINOCYCLOPROPANE-1- 79 11.6 534 1 HTRLE_PANTR RH-LIKE PROTEIN IIF (R 79 11.6 534 1 HTRLE_NAUTH SENSORY RHODOPSIN II I 79 11.6 706 1 BCL6_HUMAN B-CELL LYMPHOMA 6 PROT	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     12.6   11.7   601   1 SC2_RANT   SCRETOGRANIN II PRECU     13.6   149   1 YOK6_YEAST   PROBABLE ISOPENTENYL-D     13.6   149   1 ACCI_CUCMB   1-AMINOCYCLOPROPANE-I     140   1 RIFE_PANT   RHILE_PANT   RHILKE PROTEIN IIF (R     15   16   18 HIFE_PANT   RHILKE PROTEIN IIF (R     16   18 CLE_CHUMP   B-CELL LYMPHOMA 6 PROT     16   18 CLE_CHUMP   B-CELL LYMPHOMA 6 PROT     17   18   1 SCP1_MESAU   SYNAPTONEMAL COMPLEX P	80   11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     80   11.6   601   502_RANRI   SECRETOGRANIN II PRECU     91   11.6   149   1 VEK6_YEAST   PROBABLE ISOPENTENYL-D     91   11.6   177   1 IDI_RHOSH   PROBABLE ISOPENTENYL-D     91   11.6   131   1 ACCI_CUCMB   1-AMIROCYCLOPROPANE-I     91   11.6   534   1 HTR2_NATPH   SENSORY RHODOPSIN II F (R     79   11.6   845   1 SCPI_MESAU   BCLEL LYMPHOMA 6 PROT     91   945   1 SCPI_MESAU   SYNAPTONEMAL COMPLEX P     91   945   1 CC47_YEAST   CELL DIVISION COMPLEX P     10   11.6   11.6   12.6   12.6   13.	80   11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     80   11.7   601   1 SC2_RANAT   SCRETOGRANINI IL PRECU     91   11.6   149   1 VEK6_YEAST   PROBABLE ISOPENTENYL-D     11.6   177   1 IDI_RHOSH   PROBABLE ISOPENTENYL-D     11.6   416   1 ALCI_CHICK   1-AMINOCYCLOPROPANE-1-    11.6   416   1 ALCI_CHICK   1 RH-LIKE PROTEIN IIF (R     11.6   1 BCL6_HUMAN   B-CELL LYMPHOMA 6 PROT     11.6   845   1 SCP1_MESAU   SYNAPPONEMAL COMPLEX P     11.6   845   1 CCA7_YEAST   CELL DIVISION CONTROL     11.6   846   1 HRX_MOUSE   ZINC FINGER PROPEIN HR	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     12.0   1   SC2_RANT   SCRETOGRANIN II PRECU     13.0   1   VOK6_YEAST   PROBABLE ISOPENTENTL-D     13.0   1   1   1   1   1   1   1     14.0   1   1   1   1   1   1   1     15.0   11.6   138   1   1   1   1   1     15.0   11.6   134   1   1   1   1   1   1     15.0   11.6   1   1   1   1   1   1   1     15.0   11.6   1   1   1   1   1   1     15.0   11.6   1   1   1   1   1     16.0   1   1   1   1   1   1     17.0   11.6   1   1   1   1     18.1   1   1   1   1   1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1   10.1   10.1   10.1     19.1   10.1   10.1   10.1   10.1   10.1   10.1   10.1   10.1     19.1   10.1	80   11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     80   11.7   601   1 SC2_RANT      11.6   149   1 YEK6_YEAST   PROBABLE ISOPENTENTL-D     12.6   177   1 IDI_RHOSH   PROBABLE ISOPENTENTL-D     13.6   14.6   14.6   14.6   14.6   14.6     14.6   14.6   14.6   14.6   14.6     15.6   14.6   14.6   14.6     16.6   14.6   14.6   14.6     17.6   14.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6   14.6     18.6   14.6	80   11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     80   11.7   601   1 SC2_RANT  SCRETOGRANIN II PRECU     11.6   11.7   1 IDI_RHOSH   PROBABLE ISOPENTENYL-B     11.6	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE	80   11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE     80   11.7   601   1 SC2_RANT  SCRETORANIN II PRECU     11.6   149   1 VER6_YEAST   PROBABLE ISOPENTENYL-B     11.6   177   1 IDI_RHOSH   PROBABLE ISOPENTENYL-B     11.6   18.1   1 HTRZ_NATPH   SENSORY RHOODORSIN II F     11.6   845   1 SCPI_MESA  B-CELL LYMEHOMA 6 PROT     11.6   845   1 SCPI_MESA  SINAPTONEMAL COMPLEX P     11.6   845   1 SCPI_MESA  SINAPTONEMAL COMPLEX P     11.6   845   1 SCPI_MESA  CLL DIVISION COMPLEX P     11.6   845   1 CC47_YEAST   CLL DIVISION COMPLEX P     11.6   845   1 CC47_YEAST   CLL DIVISION COMPLEX P     11.6   1 SSE   1 RAL_SEMY   PARTORINI HR     11.4   185   1 VA_SEMY   PARTORINI CAHYDRASE VI     11.4   320   1 ACCO_PERRE I -AMINOCYCLOPROPANE-I     11.4   450   1 FLIGE_BORBU   PLAGELLAR HOOK PROTEIN     11.4   450   1 ENYZ_SALTY   OSMOLRATTY SENSOR PROTE	11.7   470   ACHP_CHICK   NEURONAL ACETYLCHOLINE	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE	11.7   470   1 ACHP_CHICK   NEURONAL ACETYLCHOLINE	11.7   470   1 ACHP_CHICK   SECRETOGRANIN   1 PRECUT     12   1   1   1   1   1   1   1   1   1

## ALIGNMENTS

RESULT

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Erythrocyte; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 93066356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                        Nadeau J.A., Zhang X., Nair H., O'Neill S.D.;

"Temporal and spatial regulation of 1-aminocyclopropane-1-carboxylate xidase in the pollination-induced senescence of orchid flowers.";

lant Physiol. 103:31-39(1993).

-!- CATALYTIC ACTIVITY: 1-4MINOCYCLOPROPANE-1-CARBOXXLATE + 02 = ETHYLENE + HCN + CO(2) + 2 H(2)O.

-!- COFACTOR: IRON AND ASCORBATE.

-!- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.

-!- SAMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF OXIDOREDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 ASKTLDTV-ENVEPENLDWESTFFLRHLPTSNISQIPDLDDDCRSTMKEFALELENLAER 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.) (ACC OXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                         Doritaenopsis sp. (Moth orchid).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Doritaenopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 9508555;
Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
Colin Y., Ruffle J.;
"Molecular genetics of chimpanzee Rh-related genes: their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MENDEL, 8019; DORSP, Acc; I.

PFAM; PF00671; Fe_Asc_oxidored; 1.

Fruit ripening; Ethylene blosynthesis; Oxidoreductase; Iron; Vitamin C; Multigene family.

SEQUENCE 327 AA; 37233 MW; D4EC83D9971059EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 103; DB 1; Length 327; 21.9%; Pred. No. 3.79e-04; Astive 23; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHLA_PANTR STANDARD; PRT; 416 AA. 02813; 01-NOY-1997 (Rel. 35, Created) 01-NOY-1997 (Rel. 35, Last sequence update) 01-NOY-1997 (Rel. 35, Last annotation update) HH-LIKE PROTEIN IA (RHESUS-LIKE PROTEIN IA) Pan troglodytes (Chimpanzee).
                                                  327 AA
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L07912; -; NOT_ANNOTATED_CDS
                                                                                                                                                          (ETHYLENE-FORMING ENZYME) (EFE)
                                                                                      26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 21.9%;
Matches 14; Conservative
                                                    STANDARD;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94269201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 LLDL 133
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91 IANI 94
                                                                                      01-JUL-1993
                                                    DORSP
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P31238;
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                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
relationship with the R-C-E-F blood group system, the chimpanzee counterpart of the human rhesus system.";
Biochem. Genet. 32:201-221(1994).
-!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           le van Kim C., Mouro I., Cherif-Zahar B., Raynal V., Cherrier C., Cartron J.-P., Colin Y.; "Molecular cloning and primary structure of the human blood group RhD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 PSFNSALLRSPIERKNAVFNTYYAVAV-SVVTAISGSSLAHPQGKISMSYMHNAVLAGGV 278
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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002161; 002162; 007618; 016355; 016147; 016235;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
BLOOD GROUP RH(D) POLYPEPTIDE (RHESUS D ANTIGEN) (RHXIII) (RH POLYPEPTIDE 2) (RHPII).
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TISSUB-BONE MARROW;
MEDLINE; 92360BSC.
le van Kim C., Cherif-Zahar B., Raynal V., Mouro I., Lopez M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 1; Length 410, Pred. No. 2.79e-02; Indels
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POTENTIAL.
BOB566734DB5E14D CRC64;
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PRINTS; PR00342; RHESUSRHD.
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S26564; S26564

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Rouillac C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;
Rouillac C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;
Rouillac C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;
Rouillac C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;

Public C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;
An. J. Hematol. 49:87-88(1995).

- I. FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
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-!- POLYMORPHISM: RHD AND RHCE ARE RESPONSIBLE FOR THE RH BLOOD GROUP SYSTEM. THE MOLECULAR BASIS OF THE TAR-RH40 BLOOD GROUP ANTIGEN IS A POLYMORPHISM IN POSITION 109.
-!- SIMILARITY: BELONGS TO THE RH FAMILY. STRONG, TO RHCE.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 93216582.
Kajil E., Umenishi F., Iwamoto S., Ikemoto S.;
Isolation of a mew cDNA clone encoding an Rh polypeptide associated
with the Rh blood group system.";
Hum. Genet. 91:157-162(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suyama K., Lunn R., Haller S., Goldstein J.; "Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform in human erythroleukemic K562 cells."; Blood 84:1975-1981(1994).
                                                                                                                                                                                                                                      "Molecular cloning of RhD cDNA derived from a gene present in RhD-positive, but not RhD-negative individuals.";
Blood 82:651-655(1993).
Cartron J.-P., Colin Y.;
"Multiple Rh messenger RNA isoforms are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *SEQUENCE FROM N.A.
MEDLINE; 95329738.
Huang C.H., Reid M.E., Chen Y.;
"Identification of a partial internal deletion in the RH locus causing the human errythrocyte D-phenotype.";
Blood 86:784-790(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (SHORT FORM 1).
MEDIINE: 94235883.
Westhoff C.M., Wylie D.E.;
"Identification of a new RhD-specific mRNA from K562 cells.";
Blood 83:3098-3100(1994).
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 93320449.
Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.
Lublin D.M.;
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MEDLINE; 94362249.
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AAB30756.1;
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                                                    splicing.";
Blood 80:1074-1078(1992)
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EMBL;
EMBL;
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S)
                                                                                         Erythrocyte, Transmembrane; Blood group antigen; Alternative splicing;
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Hirose T., Inayama S., Numa S.;
Primary structure of beta subunit precursor of calf muscle acetylcholine receptor deduced from cDNA sequence.";
Eur. J. Blochem. 144:11-17(1984).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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MISSING (IN SHORT ISOFORM 2).
L -> P (IN TAR ANTIGEN).
/FILI-VAR_006919.
M -> I.
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Pred. No. 4.06e-02;
31; Mismatches 36; Indels
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E -> G (IN REF. 4).
S -> P (IN REF. 4).
V -> A (IN REF. 4).
S -> T (IN REF. 5).
G -> V (IN REF. 5).
P -> H (IN REF. 4).
P -> H (IN REF. 4).
9136DF1A37D76B1B CRC64;
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P04758; 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CHRNB1.
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M -> I - VAR_006920.
W -> C (IN RPT
E -> C
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Local Similarity 22.6%;
hes 21; Conservative
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102
102
173
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416 AA;
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-!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL EUNCTION IN THE ERYTHROCYTE MEMBRANE.
-!- SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 PTFNSALLLNPIERKNAVFSTYYALAVSAVTAISVSSLA-HPGGKINMTYMHNAALAGGV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W., Colin Y., Ruffie J.;
"Molecular genetics of chimpanzee Rh-related genes: their relationship with the R-C-E-F blood group system, the chimpanzee counterpart of the human rheaus system.";
Biochem. Genet. 32:201-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                          -> R (IN MAC-B).
-> C (IN MAC-B).
3BFD939BEA79AF6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.89e-02;
atches 36;
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(IN MAC-B)
(IN MAC-B)
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RH-LIKE PROTEIN IIR (RHESUS-LIKE PROTEIN IIR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Mismatches
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                                                                                                                                                          Polymorphism.
BY SIMILARITY
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Pred. No. 5
                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                 MISSING
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S70343; AAB30637.1; -. PFAM; PF00909; Ammonium_transp; 1. PRINTS; PR00342; RHESUSRHD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            45672 MW;
                                                                                                                                                            Erythrocyte; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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TISSUE-BONE MARROW;
MEDLINE; 95085595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 AA;
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Q28814;
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Mol. Evol. 38:169-176(1994).
FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE RH FAMILY.
                                                                                                                                                                                                                                                      PIR; S07227; S07227.

PFAM; PF00065; neur_chan; 1.

PRINTS; PR00252; NRIONCHANNEL.

PRINTS; PR00254; NICOTINICR.

POSITE; PS00226; NEUROTALIOR.

POSITE; PS0526; NEUROTALIOR.

POSITE; PS05266; NEUROTALIOR.

POSITE; PS05266; NEUROTALIOR.

POSITE; PS05266; NEUROTALIOR.

TITANSMEMBYRANE; IONIC CHANNEL; Glycoprotein; Signal;

TITANSMEMBYRANE; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouro I., le van Kim C., Cherif-Zahar B., Salvignol I., Blancher A., Cartron J.-P., Colin Y.; "Molecular characterization of the Rh-like locus and gene transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                 SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                               MUSCLE) CHAINS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                ACETYLCHOLINE RECEPTOR PROTEIN, BETA
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Pred. No. 4.06e-02;
....matches 7; Indels
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B003D552A6701ECC CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RO-LIKE PROTEIN (RHESUS-LIKE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGNFDVA-LDINVVVSS-DGSMRWQPPGIYRSSC 152
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                                                                                                                                                                                                                                                                                                                                                                                                CHAIN.
EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
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                                                                                                                                                                                                                                         EMBL; X00962; CAA25475.1; -.
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Local Similarity 32.4%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57352
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TISSUE-BONE MARROW;
MEDLINE; 94223693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 AA;
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28849;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Biochem. Genet. 32:201-221(1994).

-!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE RH FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. (RHESUS-LIKE PROTEIN)
11-NOV-1997 (RHESUS-LIKE 
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TISSUE-BONE MARROW:
MEDLINE; 95085959.
Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
Colin Y., Ruffle J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C055D7CC8B4A0420 CRC64;
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PFAM; PF00909; Ammonium_transp; 1.
Erythrocyte; Transmembrane.
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PRINTS; PR00342; RHESUSRHD.
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                                                                                                      EMBL; L37050; AAA65624.1; -.
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416 AA;
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                                                                                                                                                       220 PSFNSALLTNPIERKNAVFNTYYALAVSTVTAISVSSLAHPQGKINMTYMHNAVLAGGVA 279
                                                                                                                                                                     HO M.N., Hill K.J., Lindorfer M.A., Stevens T.H.; "Isolation of vacuolar membrane H(+)-ATPase-deficient yeast mutants; the VMA5 and VMA4 genes are essential for assembly and activity of
                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beltran C., Kopecky J., Pan Y.-C.E., Nelson H., Nelson N.; "Cloning and mutational analysis of the gene encoding subunit C of
                                                                                                                                                                                                                                                                                                                                             (V-ATPASE C SUBUNIT)
                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James C.M., Gent M.E., Indge K.J., Oliver S.G.; "Sequence analysis of a 10 kb fragment of yeast chromosome XI identifies the SMY1 locus and reveals sequences related to a psplicing factor and vacuolar ATPase subunit C plus a number of
                                                                                          Score 86; DB 1,
"~ed. No. 2.55e-01;
"~hes 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
3CFD25B38033AB6A CRC64;
                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34)
VAPPASE 42 KDA SUBUNIT).
WMA5 OR VAT3 OR VATC OR YKLO
                                                                                                                                                                                                                                                                                 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 99-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE; 93107006.
   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                       280 VGTSCHLISSPWLAMVLGLVAGLISIGGA 308
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                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yeast vacuolar H(+)-ATPase.";
J. Biol. Chem. 267:774-779(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 268:221-227(1993)
                                                                             MM;
96
144
186
228
257
306
38417 M
                                                                                                     12.6%;
21.3%;
                                                                                                                  Local Similarity 21.3%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the vacuolar H(+)-ATPase.
                                                                                                                                                                                                                                                                                  STANDARD;
   76
124
166
208
237
286
353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Pohl F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94262328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 92112808
                                                                                                                                                                                                                                                                  RESULT 9
ID VATC_YEAST
AC P31412;
                 TRANSMEM
TRANSMEM
TRANSMEM
                                                    TRANSMEM
TRANSMEM
SEQUENCE
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                                                                                                       Query Match
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A MEDIANIE 9128693.

A Rothe B., Rothe B., Rogentin P., Schauer R.;

Rothe B., Rothe B., Rogentin P., Schauer R.;

The stalidase gene from Clostridium septicum: cloning, sequencing,

The stalidase gene from Clostridium septicum:

The stalidase gene from Clostridium septicum of conserved

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATALYTANDFILISLPQNAQPVTA -> MLNLLR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
01-0CT-1994 (Rel. 30, Last annotation update)
Clostridium septicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 12.6%; Score 86; DB 1; Length 392; Local Similarity 24.1%; Pred. No. 2.55e-01; es 21; Conservative 24; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCD1B814046C377E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Glycosidase; Periplasmic; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1014 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF. 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 DVRATYANYNSAKTNLAAAERKKTGDL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 ECKTRAQOFVSTKINLDDHIANIDGTL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Hydrogen ion transport.
CONFLICT 1 25 MATAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AA; 44188 MW;
                                                                                                                                                                                                                                                                                                                                               EMBL; X75560; CAA53237.1; -... 228080; CAA81917.1; -... 37905; S37905. S17905. PIR; S39118; S3
                                                                                                                                                                                                                                                                                                               EMBL; M77143; AAA34440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X63266; CAA44916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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HSSP; Q02834; 1EUS.
PFAM; PF02012; BNR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-NC 0054714;
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P29767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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-!- CATALYTIC ACTIVITY: DONOR + H(2)0(2) = OXIDIZED DONOR + 2 H(2)0.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, KIDNEY AND LIVER. MODERATE EXPRESSION IN BRAIN AND STOMACH. VERY LOW LEVELS IN INTESTINE.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STAILN-BAIB/C; TISSUE-SKIN;
MEDLINE; 97419117.
Minz B., Frank S., Huebner G., Olsen E., Werner S.;
Manz B., Frank S., Huebner G., Olsen E., Werner S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
STRAIN-DBA/2J, C57BL/6J, AND C3H/FEJ; TISSUE-LIVER, AND KIDNEY;
MEDLINE; 97349116.
Iakoubova O.A., Pacella L.A., Her H., Beier D.R.;
"LTW4 protein on mouse chromosome 1 is a member of a family of antioxidant proteins";
Genomics 42:474-478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
Lee T.H., Yu S.L., Kim S.Y., Kang S.W., Rhee S.G., Seong J.K.,
                                                                                                                                                                         ä;
                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (NONSELENIUM GLUTATHIONE PEROXIDASE) (1-CYS PEROXIREDOXIN) (1-CYS PRX).
POTENTIAL.
SIALIDASE.
BNR MOTIF.
BNR MOTIF.
BNR MOTIF.
MW; C4F49233473A2FAD CRC64;
                                                                                                                                      Score 86; DB 1; Length 1014;
Pred. No. 2.55e-01;
20; Mismatches 12; Indels
                                                                                                                                                                                                           401 Y-TTKDGTVLASIDVRKGGGHDAPN-NIDTGIKRSTDGGVTWDEGKII 446
                                                                                                                                                                                                                          223 AA
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF004670; AAC53277.1; -.
EMBL; Y12883; CAA73383.1; -.
EMBL; AF093822; AAC63376.1; -.
HSSP; P30041; 1PRX.
SWISS-2DPAGE; 008709; MOUSE.
MGD; MGI:894320; AOP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 326:579-585(1997).
1 26
27 1014
431 442
563 574
527 638
700 711
1014 AA; 110652 M
                                                                                                                                         12.68;
                                                                                                                                                      Best Local Similarity 27.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         during wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            AOP2_MOUSE
                                                                                                        SEQUENCE
                                                                                                                                         Query Match
                   CHAIN
REPEAT
REPEAT
REPEAT
   SIGNAL
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                                                                                        REPEAT
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-!- CATALYTIC ACTIVITY: DONOR + H(2)O(2) - OXIDIZED DONOR + 2 H(2)O.
-!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    730041; P32077; FRI; 643 AA.
1-APR-1993 (Rel. 25, Created)
10-CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 34, Last annotation update)
ANTIOXIDANT PROFERN 2 (EC 1.11.1.7) (24 KDA PROFEIN) (LIVER 2D PAGE SPOT 40) (RED BLOOD CELLS PAGE SPOT 12).
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F., Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R., Appel R.D., Hughes G.J., "Human liver protein map: a reference database established by microsequencing and gel comparison."; Electrophoresis 13:992-1001(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Golda C., Hughes G.J., Frutiger S., Paquet N., Bairoch A., Basquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C., Salant L., Hochstrasser D.F.; Blasma and red blood cell protein maps: update 1993."; Electrophoresis 14:1223-1231(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98246415.
Choi H.J., Kang S.W., Yang C.H., Rhee S.G., Ryu S.E.;
"Crystal structure of a novel human peroxidase enzyme at 2.0-A
                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                     33 GILFSHPRDFTPVC-TTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLA 80
                                                                                                                                                                                                                                                                               Length 223;
                                                                                                                                                        Score 85; DB 1; Length 223;
Pred. No. 3.65e-01;
14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miyajima N.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
                                                                46 BY SIMILARITY.
123 D -> A (IN C57BL/6J).
24739 MW; A4F2B1E36180BBCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            223 AA
PFAM; PF00578; Ahpc-TSA; 1.
Oxidoreductase; Peroxidase; Antioxidant.
INIT_MET 0 0 0
ACT_ENT 46 46 BY SIMILARI
VARIANT 123 123 D -> A (IN
SEQUENCE 223 AA; 24739 MW; A4F2BIB36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D14662; BAA03496.1; -. PDB; 1PRX; 17-JUN-98. SWISS-2DPAGE; P30041; HUMAN. PFAM; PFO0578; AhpC-TSA; 1.
                                                                                                                                                        12.4%;
Similarity 30.6%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE OF 1-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE OF 1-12.
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-ERYTHROCYTE;
MEDLINE; 94147970.
                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93162045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resolution.";
                                                                                                                                                                                                                                                                                                                                                                                            AOP2_HUMAN
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PIR; $13873; $13873.
PIRM; PF00065; neur_chan; 1.
PRINTS; PR00254; NRTONCHANNEL.
PRINTS; PR00254; NICOTINICR.
PROSTER; PR00264; NICOTINICR.
TROSTER; PROSUS6; NEURONEL ON CHANNEL; 1.
TROSPITE; PROSUS6; MEMBLANEL; 1.
Transmembrane; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELIA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSCLE) CHAINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN.
                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                                                                                         33 GILFSHPRDFTPVC-TTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLA 80
                                                                                                                                                     18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                               24904 MW; 0B42C96F5CEBEFFC CRC64;
Oxidoreductase; Peroxidase; Antioxidant; 3D-structure.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                      Score 85; DB 1; L
Pred. No. 3.65e-01;
14; Mismatches 18
                                                                                                                                                                                                                                                                                                                               501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
POTENTIAL.
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                                                                                                            12.4%;
                                                                                                        Query Match 12.4%;
Best Local Similarity 30.6%;
Matches 15; Coffservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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MEDLINE; 91099317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHRNB1 OR ACRB.
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                      INIT_MET
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                           T 13
ACHB_RAT
P25109;
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DISULFID
CARBOHYD
MOD_RES
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97026281.
Engel A.G., Ohno K., Milone M., Wang H.-L., Nakano S., Bouzat C.,
Pruitt J.N. II, Hutchinson D.O., Brengman J.M., Bren N., Sieb J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sine S.M.;
"New mutations in acetylcholine receptor subunit genes reveal
heterogeneity in the slow-channel congenital myasthenic syndrome.";
Hum. Mol. Genet. 5:1217-1227 (1996).
- FUNCTION: AFFER BINDIA ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gomez C.M., Maselli R., Gammack J., Lasalde J., Tamamizu S.,
Cornblath D.R., Lehar M., McNamee M., Kuncl R.W.;
"A beta-subunit mutation in the acetylcholine receptor channel gate
causes severe slow-channel syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DISEASE: DEFECTS IN ACHE ARE ONE OF THE CAUSES OF THE SLOW-
CHANNEL CONGENITAL MYASTHENIC SYNDROME (SCCMS).
SIMILARITY: BELONGS TO THE LICAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                              ë,
                                                                                                                                                                                                                                                                                                                                                                                                                   Beeson D.M.W., Brydson M., Newsom-Davis J.; "Nucleotide sequence of human muscle acetylcholine receptor
                                              Length 501;
(BY SIMILARITY).
2E7DD6AAD1D9364D CRC64;
                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
HRNB1 OR CHRNB OR ACHRB.
                                            Score 85; DB 1; Le
Pred. No. 3.65e-01;
                                                                                                                                                                                                         501 AA.
                                                                            14; Mismatches
                                                                                                            120 DGNFDVA-LDINVVV-SFEGSVRWQPPGLYRSSC 151
                                                                                                                              26 NGGYNTSSIDLNSVIENVDGSLKWQPSN-FIETC 58
                                              Score 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 17:4391-4391(1989).
                                                                                                                                                                                                       PRT;
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PRINTS; PR00252; NRIONCHANNEL
             57026 MW;
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                                              12.48;
                                                           Local Similarity 29.4%;
les 10; Conservative
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MIM; 100710; -.
MIM; 601462; -.
PFAM; PF00065; neur_c
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ACHB_HUMAN
             SEQUENCE
                                              Query Match
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Buonanno A., Mudd J., Merlie J.P.;

Buonanno A., Mudd J., Merlie J.P.;

Buonanno A., Mudd J., Merlie J.P.;

Isolation and characterization of the beta and epsilon subunit genes of mouse muscle acetylcholine receptor.";

J. Biol. Chem. 264:7611-7616(1989).

-: FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTERNSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS. TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Phosphorylation; Disease mutation.

1 23
SIGNAL
1 24
SOI
ACETYLCHOLINE RECEPTOR PROTEIN, BETA
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"A universal oligonucleotide probe for acetylcholine receptor genes. Selection and sequencing of cDNA clones for the mouse muscle beta subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY
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/FTId=VAR_000288.
F8255BDE366A2A84 CRC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NAR-1987 (Rel. 15, Last annotation update)
ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
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/FTId-VAR_000287.
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CHAIN.
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                                        EMBL; M14537; AAA37154 1; -.
EMBL; J04699; AAA371561; -.
EMBL; J04699; AAA371561; -.
EMBL; J04699; AAA371561; -.
EMBL; J04699; AAA371561; -.
PTR, ABC 187890; ACRB.
PRINTS; PR00252; NRIONCHANNEL.
PRINTS; PR00252; NRIONCHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Phosphorylation.
SIGNAL
24 501 ACETYLCHOLINE RECEPTOR PROTEIN, BETA
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PROBABLE.
PHOSPHORYLATION (BY TYR-KINASES)
PHOSPHORYLARITY).
787BDDA90EBB0EF2 CRC64;
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Pred. No. 3.65e-01;
14; Mismatches 7; Indels
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EXTRACELLULAR.
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Best Local Similarity 29.4%;
Matches 10; Conservative
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